Sequence Alignment #1

```
<!--StartFragment-->RESULT 2
TSHB_CANFA
ID   TSHB_CANFA              Reviewed;          138 AA.
AC   P54828;
DT   01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
DT   01-OCT-1996, sequence version 1.
DT   23-OCT-2007, entry version 42.
DE   Thyrotropin subunit beta precursor (Thyroid-stimulating hormone
DE   subunit beta) (TSH-beta) (TSH-B) (Thyrotropin beta chain).
GN   Name=TSHB;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Caniformia; Canidae;
OC   Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Pituitary;
RA   Kania S.A., Frank L.A.;
RL   Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Indispensable for the control of thyroid structure and
CC       metabolism.
CC   -!- SUBUNIT: Heterodimer of a common alpha chain and a unique beta
CC       chain which confers biological specificity to thyrotropin,
CC       lutropin, follitropin and gonadotropin.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the glycoprotein hormones subunit beta
CC       family.
CC   -----------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----------------------------------------------------------------------
DR   EMBL; U51644; AAA97410.1; -; mRNA.
DR   RefSeq; NP_001003290.1; -.
DR   UniGene; Cfa.3841; -.
DR   HSSP; P01233; 1HCN.
DR   Ensembl; ENSCAFG00000009713; Canis familiaris.
DR   GeneID; 403973; -.
DR   KEGG; cfa:403973; -.
DR   InterPro; IPR006208; Cys_knot.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   PANTHER; PTHR11515; Gly_hormoneB; 1.
DR   Pfam; PF00007; Cys_knot; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
PE   2: Evidence at transcript level;
KW   Glycoprotein; Hormone; Secreted; Signal.
FT   SIGNAL        1     20       By similarity.
FT   CHAIN        21    132       Thyrotropin subunit beta.
FT                                /FTId=PRO_0000011742.
FT   PROPEP      133    138       By similarity.
FT                                /FTId=PRO_0000011743.
FT   CARBOHYD     43     43       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID     22     72       By similarity.
FT   DISULFID     36     87       By similarity.
FT   DISULFID     39    125       By similarity.
FT   DISULFID     47    103       By similarity.
FT   DISULFID     51    105       By similarity.
FT   DISULFID    108    115       By similarity.
SQ   SEQUENCE   138 AA;  15666 MW;  A3298FFDDF6A005F CRC64;

  Query Match             94.2%;  Score 632;  DB 1;  Length 138;
  Best Local Similarity   94.9%;  Pred. No. 6.6e-58;
  Matches  112;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 FCFPTEYMMHVERKECAYCLTINTTICAGYCMTRDINGKLFLPKYALSQDVCTYRDFLYK 60
              ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||:||
Db         21 FCFPTEYTMHVERKECAYCLTINTTICAGYCMTRDINGKLFLPKYALSQDVCTYRDFMYK 80

Qy         61 TVEIPGCPHHVTPYFSYPVAVSCKCGKCNTDYSDCIHEAIKTNDCTKPQKSDVVGVSI 118
              |||||||| ||||||||||||||||||||||||||||||||||| ||||||| ||| ||
Db         81 TVEIPGCPRHVTPYFSYPVAVSCKCGKCNTDYSDCIHEAIKTNYCTKPQKSYVVGFSI 138
<!--EndFragment-->
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